

In the claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

Please cancel claims 1-31 and add the following new claims.

1-31. (Canceled)

32. (new) A method of detecting the silencing of a target gene in an organism, wherein said silencing is initiated by introduction of an exogenous nucleic acid, which method comprises the steps of:

(i) obtaining a sample of material from said organism,

(ii) producing a nucleic acid extract from said sample,

(iii) analyzing said extract such as to determine the presence or absence of short RNA molecules which are 21-25 nucleotides in length (SRMs) in said extract,

(iv) characterizing any SRMs which are present in said extract such as to determine sequence identity or similarity with said target gene, and

(v) correlating the presence of said SRMs having sequence identity or similarity with said target gene in the extract with the occurrence of gene silencing in said organism.

33. (new) A method in accordance with claim 1, wherein the organism is a plant.

34. (new) A method in accordance with claim 1, wherein the organism is a nematode.

35. (new) A method in accordance with claim 1, wherein the organism is a mammal.

36. (new) A method in accordance with claim 1 wherein the SRMs are short anti-sense RNA molecules (SARMs).

37. (new) A method in accordance with claim 1 wherein the SRMs are short sense RNA molecules (SSRMs).

38. (new) A method in accordance with claim 1, wherein the gene silencing is post-transcriptional gene silencing (PTGS).

39. (new) A method in accordance with claim 1, wherein the silencing of said target gene in the organism is associated with pathogen derived resistance.

40. (new) A method in accordance with claim 1, wherein the silencing of said target gene in the organism is associated with modification of a specific trait by co-suppression of the target gene.

41. (new) A method of identifying a silenced target gene in an organism in which gene silencing is detected as claimed in claim 1, which method further comprises the steps of:

(vi) preparing a library of genes from said organism, and

(vii) identifying those genes in said library which share sequence identity or similarity with any SRMs which are present in the extract as being genes which are silenced in the organism.

42. (new) A process for isolating one or more RNA molecules associated with target gene silencing from a sample of material from an organism, wherein the RNA molecules are SRMs which share sequence identity with the target gene, and wherein said silencing is initiated by introduction of an exogenous nucleic acid, which process comprises the steps of:

(a) producing a nucleic acid extract from said sample,
(b) purifying said extract to produce purified RNA molecules which are 21-25 nucleotides in length by carrying out at least one purification step selected from the following steps (i) filtration; (ii) differential precipitation (iii) ion exchange chromatography, such as to isolate said SRMs.

43. (new) A process according to claim 42 which further comprises the step of separating the purified RNA molecules according to size by electrophoresis through a gel, which gel is a 15% polyacrylamide gel containing 7M urea as a denaturant and TBE (0.5x) as a buffer.

44. (new) A process according to claim 43 which further comprises the step of transferring the RNA molecules on the gel to a hybridization membrane by electrophoresis.

45. (new) A process according to claim 44 which further comprises the step of labeling RNA molecules on the hybridization membrane using a radioactive probe obtained from a single stranded RNA molecule transcribed in vitro from a plasmid DNA template.

46. (new) A process for isolating a silencing agent comprising SRMs for a target gene from an organism, which process comprises the steps of:

(i) silencing said target gene in said organism, wherein said silencing is initiated by introduction of an exogenous nucleic acid,

(ii) obtaining a sample of material from said organism,

(iii) performing a process in accordance with claim 42 to isolate said SRMs.

47. (new) A method according to claim 1 wherein the target gene is an animal gene selected from the group consisting of: a gene involved in apoptosis; a gene involved in cell-cycle regulation; and a gene involved in a neurological process.

48. (new) A method as claimed in claim 1, wherein said short RNA molecules are between 23 and 25 nucleotides in length.

49. (new) A method as claimed in claim 1, wherein said short RNA molecules are 25 nucleotides in length.